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☐ 1: Q96JB6. Lysyl oxidase hom...[gi:20177960]

BLink, Domains, Links

LOCUS Q96JB6 756 aa linear PRI 15-JUN-2004

DEFINITION Lysyl oxidase homolog 4 precursor (Lysyl oxidase-like protein 4)  
(Lysyl oxidase related protein C).

ACCESSION Q96JB6

VERSION Q96JB6 GI:20177960

DBSOURCE swissprot: locus LOL4\_HUMAN, accession Q96JB6;

class: standard.

extra accessions:Q96DY1,Q96PC0,Q9H6T5,created: Feb 28, 2003.

sequence updated: Feb 28, 2003.

annotation updated: Jun 15, 2004.

xrefs: gi: 14669470, gi: 14669471, gi: 17861371, gi: 17861372, gi: 16660130, gi: 16660131, gi: 14043078, gi: 14043079, gi: 15341930, gi: 15341931, gi: 10438090, gi: 10438091

xrefs (non-sequence databases): GenewHGNC:17171, MIM 607318, InterProIPR001695, InterProIPR001190, PfamPF01186, PfamPF00530, PRINTSPR00074, PRINTSPR00258, ProDomPD013887, SMARTSM00202, PROSITEPS00926, PROSITEPS00420, PROSITEPS50287

KEYWORDS Oxidoreductase; Copper; Glycoprotein; Repeat; Signal; LTQ.

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1 (residues 1 to 756)

AUTHORS Ito,H., Akiyama,H., Iguchi,H., Iyama,K., Miyamoto,M., Ohsawa,K. and Nakamura,T.

TITLE Molecular cloning and biological activity of a novel lysyl oxidase-related gene expressed in cartilage

JOURNAL J. Biol. Chem. 276 (26), 24023-24029 (2001)

MEDLINE 21316447

PUBMED 11292829

REMARK SEQUENCE FROM N.A.

TISSUE=Testis

REFERENCE 2 (residues 1 to 756)

AUTHORS Maki,J.M., Tikkanen,H. and Kivirikko,K.I.

TITLE Cloning and characterization of a fifth human lysyl oxidase isoenzyme: the third member of the lysyl oxidase-related subfamily with four scavenger receptor cysteine-rich domains

JOURNAL Matrix Biol. 20 (7), 493-496 (2001)

MEDLINE 21550107

PUBMED 11691589

REMARK SEQUENCE FROM N.A.

REFERENCE 3 (residues 1 to 756)

AUTHORS Asuncion,L., Fogelgren,B., Fong,K.S., Fong,S.F., Kim,Y. and Csiszar,K.

TITLE A novel human lysyl oxidase-like gene (LOXL4) on chromosome 10q24 has an altered scavenger receptor cysteine rich domain

JOURNAL Matrix Biol. 20 (7), 487-491 (2001)

MEDLINE 21550106

PUBMED 11691588

REMARK SEQUENCE FROM N.A.  
TISSUE=Placenta

REFERENCE 4 (residues 1 to 756)

AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Kettelman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.

TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

MEDLINE [22388257](#)

PUBMED [12477932](#)

REMARK SEQUENCE FROM N.A.  
TISSUE=Eye

REFERENCE 5 (residues 1 to 756)

AUTHORS Ota,T., Suzuki,Y., Nishikawa,T., Otsuki,T., Sugiyama,T., Irie,R., Wakamatsu,A., Hayashi,K., Sato,H., Nagai,K., Kimura,K., Makita,H., Sekine,M., Obayashi,M., Nishi,T., Shibahara,T., Tanaka,T., Ishii,S., Yamamoto,J., Saito,K., Kawai,Y., Isono,Y., Nakamura,Y., Nagahari,K., Murakami,K., Yasuda,T., Iwayanagi,T., Wagatsuma,M., Shiratori,A., Sudo,H., Hosoiri,T., Kaku,Y., Kodaira,H., Kondo,H., Sugawara,M., Takahashi,M., Kanda,K., Yokoi,T., Furuya,T., Kikkawa,E., Omura,Y., Abe,K., Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M., Ninomiya,K., Ishibashi,T., Yamashita,H., Murakawa,K., Fujimori,K., Tanai,H., Kimata,M., Watanabe,M., Hiraoka,S., Chiba,Y., Ishida,S., Ono,Y., Takiguchi,S., Watanabe,S., Yosida,M., Hotuta,T., Kusano,J., Kanehori,K., Takahashi-Fujii,A., Hara,H., Tanase,T.O., Nomura,Y., Togiya,S., Komai,F., Hara,R., Takeuchi,K., Arita,M., Imose,N., Musashino,K., Yuuki,H., Oshima,A., Sasaki,N., Aotsuka,S., Yoshikawa,Y., Matsunawa,H., Ichihara,T., Shiohata,N., Sano,S., Moriya,S., Momiyama,H., Satoh,N., Takami,S., Terashima,Y., Suzuki,O., Nakagawa,S., Senoh,A., Mizoguchi,H., Goto,Y., Shimizu,F., Wakebe,H., Hishigaki,H., Watanabe,T., Sugiyama,A., Takemoto,M., Kawakami,B., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukuzumi,Y., Fujimori,Y., Komiyama,M., Tashiro,H., Tanigami,A., Fujiwara,T., Ono,T., Yamada,K., Fujii,Y., Ozaki,K., Hirao,M., Ohmori,Y., Kawabata,A., Hikiji,T., Kobatake,N., Inagaki,H., Ikema,Y., Okamoto,S., Okitani,R., Kawakami,T., Noguchi,S., Itoh,T., Shigeta,K., Senba,T., Matsumura,K., Nakajima,Y., Mizuno,T., Morinaga,M., Sasaki,M., Togashi,T., Oyama,M., Hata,H., Watanabe,M., Komatsu,T., Mizushima-Sugano,J., Satoh,T., Shirai,Y., Takahashi,Y., Nakagawa,K., Okumura,K., Nagase,T., Nomura,N., Kikuchi,H., Masuho,Y., Yamashita,R., Nakai,K., Yada,T., Nakamura,Y., Ohara,O., Isogai,T. and Sugano,S.

TITLE Complete sequencing and characterization of 21,243 full-length human cDNAs

JOURNAL Nat. Genet. 36 (1), 40-45 (2004)  
 PUBMED [14702039](#)  
 REMARK SEQUENCE OF 492-756 FROM N.A.  
 COMMENT

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[FUNCTION] May modulate the formation of a collagenous extracellular matrix.  
 [COFACTOR] Copper and LTQ (By similarity).  
 [SUBCELLULAR LOCATION] Extracellular (Potential).  
 [TISSUE SPECIFICITY] Expressed in many tissues, the highest levels among the tissues studied being in the skeletal muscle, testis and pancreas. Expressed in cartilage.  
 [PTM] The lysine tyrosylquinone cross-link (LTQ) is generated by condensation of the epsilon-amino group of a lysine with a topaquinone produced by oxidation of tyrosine.  
 [SIMILARITY] Belongs to the lysyl oxidase family.  
 [SIMILARITY] Contains 4 SRCR domains.

FEATURES	Location/Qualifiers
source	1..756 /organism="Homo sapiens" /db_xref="taxon:9606"
gene	1..756 /gene="LOXL4" /note="synonym: LOXC"
Protein	1..756 /gene="LOXL4" /product="Lysyl oxidase homolog 4 precursor" /EC_number="1.4.3.-"
Region	1..24 /gene="LOXL4" /region_name="Signal" /note="Potential."
Region	3 /gene="LOXL4" /region_name="Conflict" /note="W -> R (in Ref. 4)."
Region	25..756 /gene="LOXL4" /region_name="Mature chain" /note="Lysyl oxidase homolog 4."
Region	32..133 /gene="LOXL4" /region_name="Domain" /note="SRCR 1."
Region	32..132 /gene="LOXL4" /region_name="Scavenger receptor Cys-rich" /note="SR" /db_xref="CDD:178"
Region	101 /gene="LOXL4" /region_name="Conflict" /note="R -> Q (in Ref. 4)."
Region	159..287 /gene="LOXL4"

Region /region\_name="Domain"  
/note="SRCR 2."  
174..286  
/gene="LOXL4"  
/region\_name="Scavenger receptor Cys-rich"  
/note="SR"  
/db\_xref="CDD:178"

Site 198  
/gene="LOXL4"  
/site\_type="glycosylation"  
/note="N-linked (GlcNAc...) (Potential)."

Region 311..411  
/gene="LOXL4"  
/region\_name="Domain"  
/note="SRCR 3."

Region 311..411  
/gene="LOXL4"  
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/note="SR"  
/db\_xref="CDD:178"

Region 405  
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/note="D -> A (in Ref. 4)."

Region 421..529  
/gene="LOXL4"  
/region\_name="Domain"  
/note="SRCR 4."

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/note="SR"  
/db\_xref="CDD:178"

Region 493  
/gene="LOXL4"  
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/note="S -> G (in Ref. 3)."

Region 533..736  
/gene="LOXL4"  
/region\_name="Lysyl oxidase"  
/note="Lysyl oxidase"  
/db\_xref="CDD:7932"

Region 533..736  
/gene="LOXL4"  
/region\_name="Domain"  
/note="Lysyl-oxidase like."

Region 539  
/gene="LOXL4"  
/region\_name="Conflict"  
/note="A -> T (in Ref. 3)."

Region 542  
/gene="LOXL4"  
/region\_name="Conflict"  
/note="V -> A (in Ref. 3)."

Site 611  
/gene="LOXL4"  
/site\_type="metal-binding"  
/note="Copper (Potential)."

Site 613  
/gene="LOXL4"

Site /site\_type="metal-binding"  
/note="Copper (Potential)."  
615  
/gene="LOXL4"  
/site\_type="metal-binding"  
/note="Copper (Potential)."  
Site 629  
/gene="LOXL4"  
/site\_type="glycosylation"  
/note="N-linked (GlcNAc...) (Potential)."  
Bond bond(638,674)  
/gene="LOXL4"  
/bond\_type="xlink"  
/note="Lysine tyrosylquinone (Lys-Tyr) (By similarity)."  
Site 674  
/gene="LOXL4"  
/site\_type="modified"  
/note="2',4',5'-topaquinone (By similarity)."  
Region 703  
/gene="LOXL4"  
/region\_name="Conflict"  
/note="Y -> H (in Ref. 3)."

## ORIGIN

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121 dcshsedvgv ichprrrhrgy lsetvsnalq pqgrrleevr lkpilasakq hspvtegave
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241 knsfwihqvt clgtephman cqvqvaparg klrpacpggm havvscvagg hfrppktkppq
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361 lfgarlgqgl gpihlsevr c rgyertlsdc palegsqngc qhendaavrc nvpmgmfgnq
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541 lvqetayled rplsqlycah eencslksad hmdwpygyrr llrfstqiyn lgrtdfrpkt
601 grdswvwhqc hrhyhsievf thydlitlng skvaeghkas fcledtncpt glqrryacan
661 fgeggvtvgc wdyrhdidc qwvditdvgp gnyifqvivn phyevaesdf snnmlqcrck
721 ydghrvwlhn chtgnsypan aelsleqeqr lrnnli
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Oct 4 2004 14:35:49